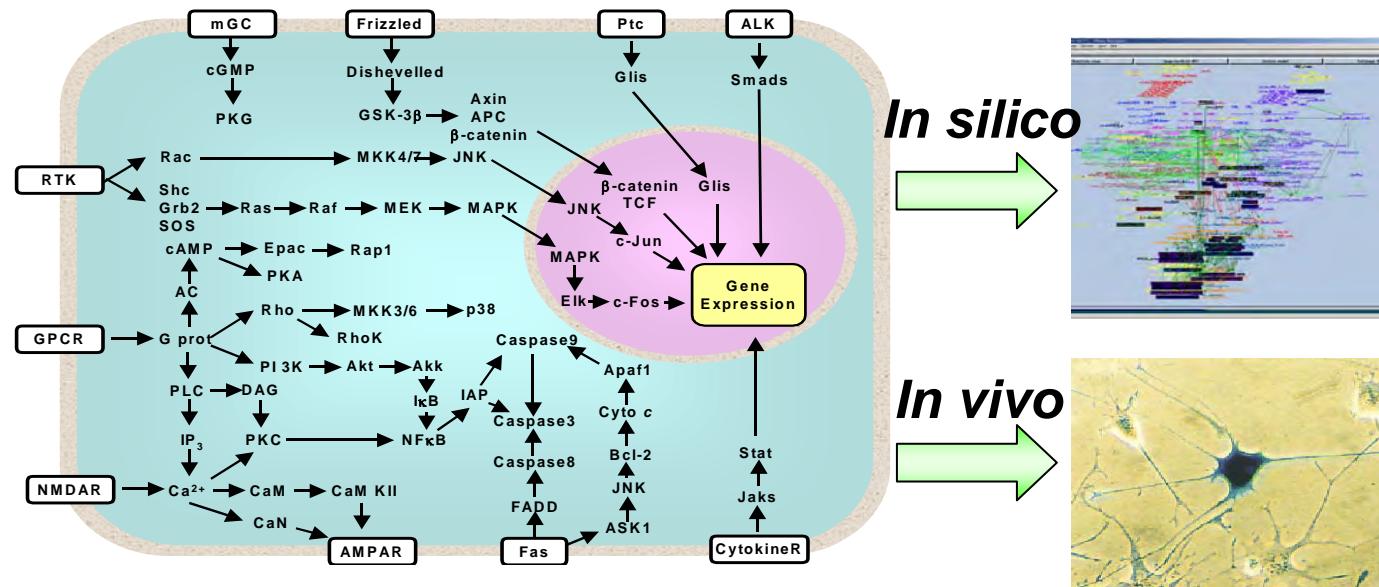


Temporal coding of ERK signaling networks



Shinya Kuroda

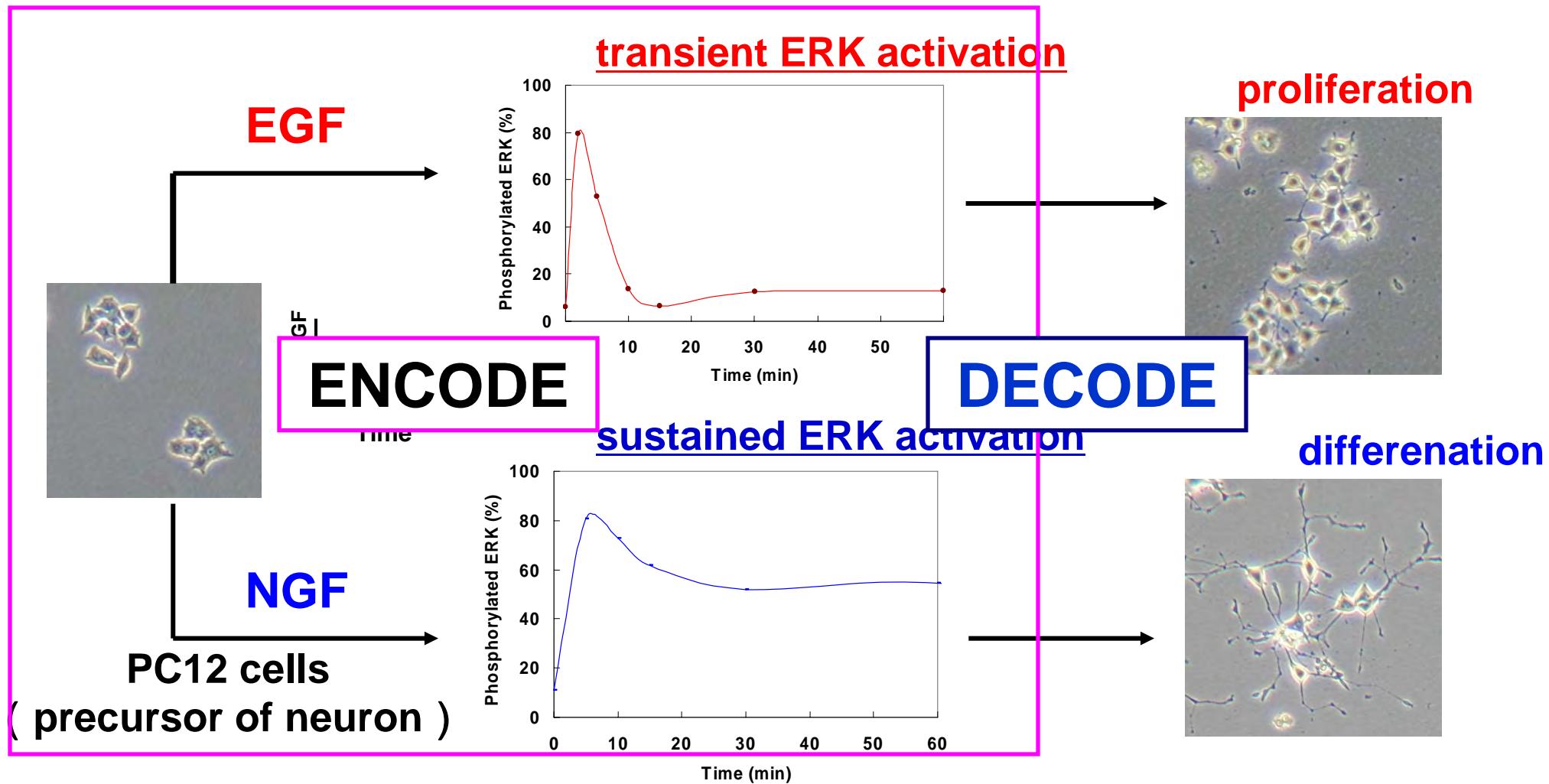
Biophysics and Biochemistry
University of Tokyo

Kuroda Lab

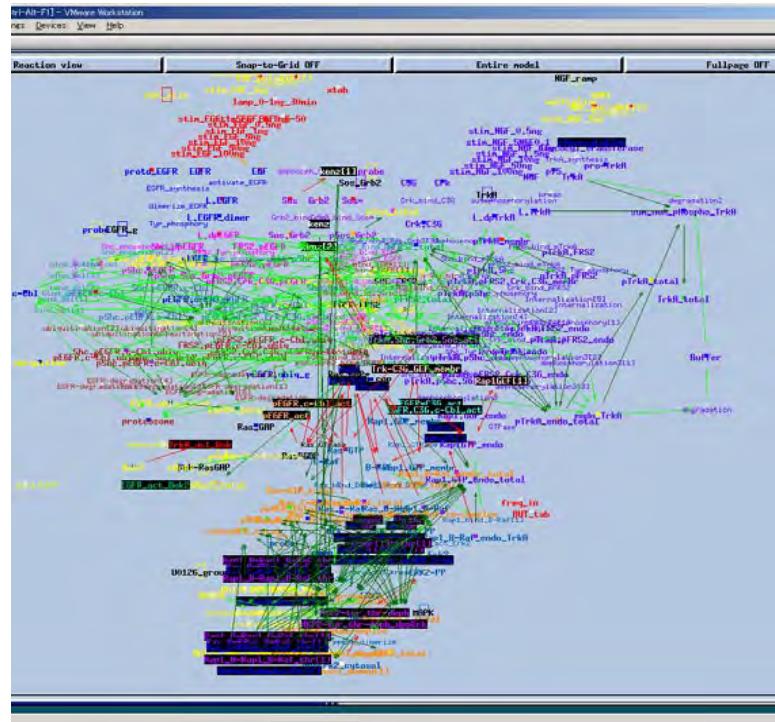
Undergraduate Program for Bioinformatics and Systems Biology, Graduate School of Information Science and Technology, University of Tokyo, JAPAN

Cell Fate Determination

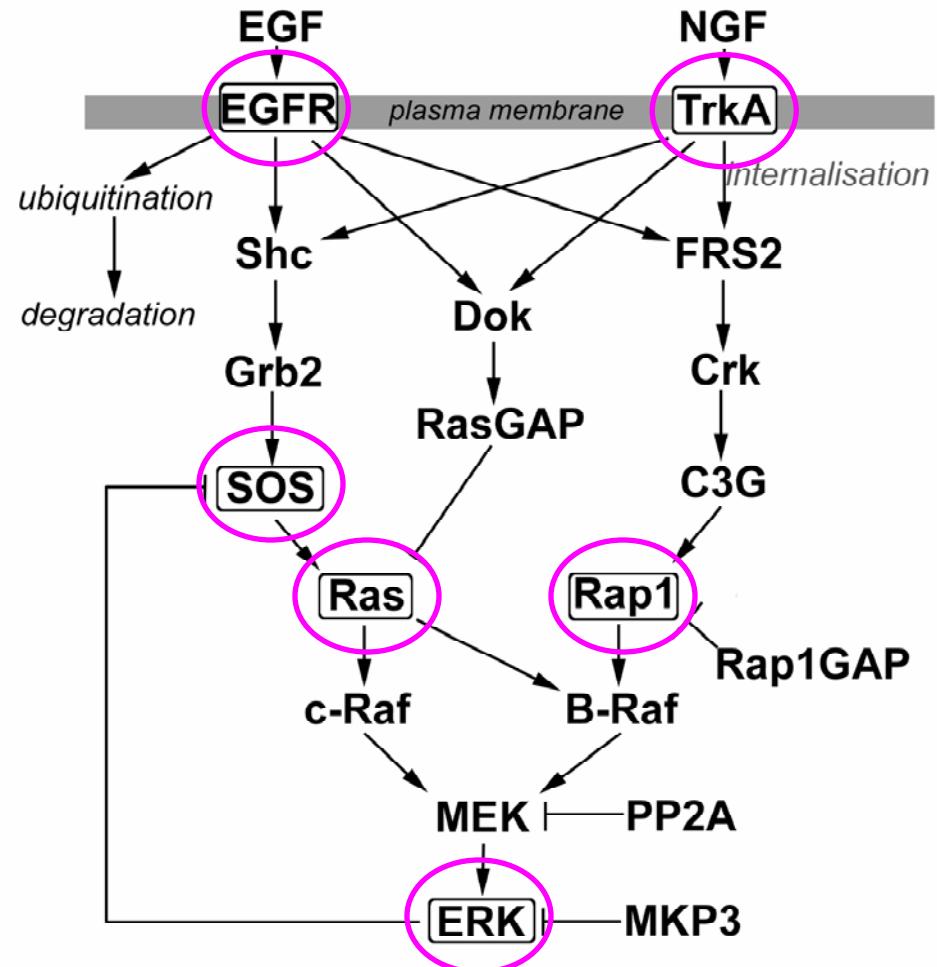
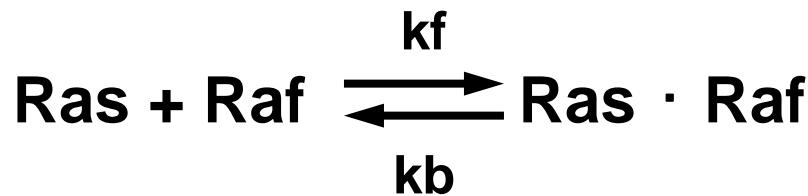
Temporal coding of ERK activation for growth and differentiation



Kinetic simulation model of ERK network

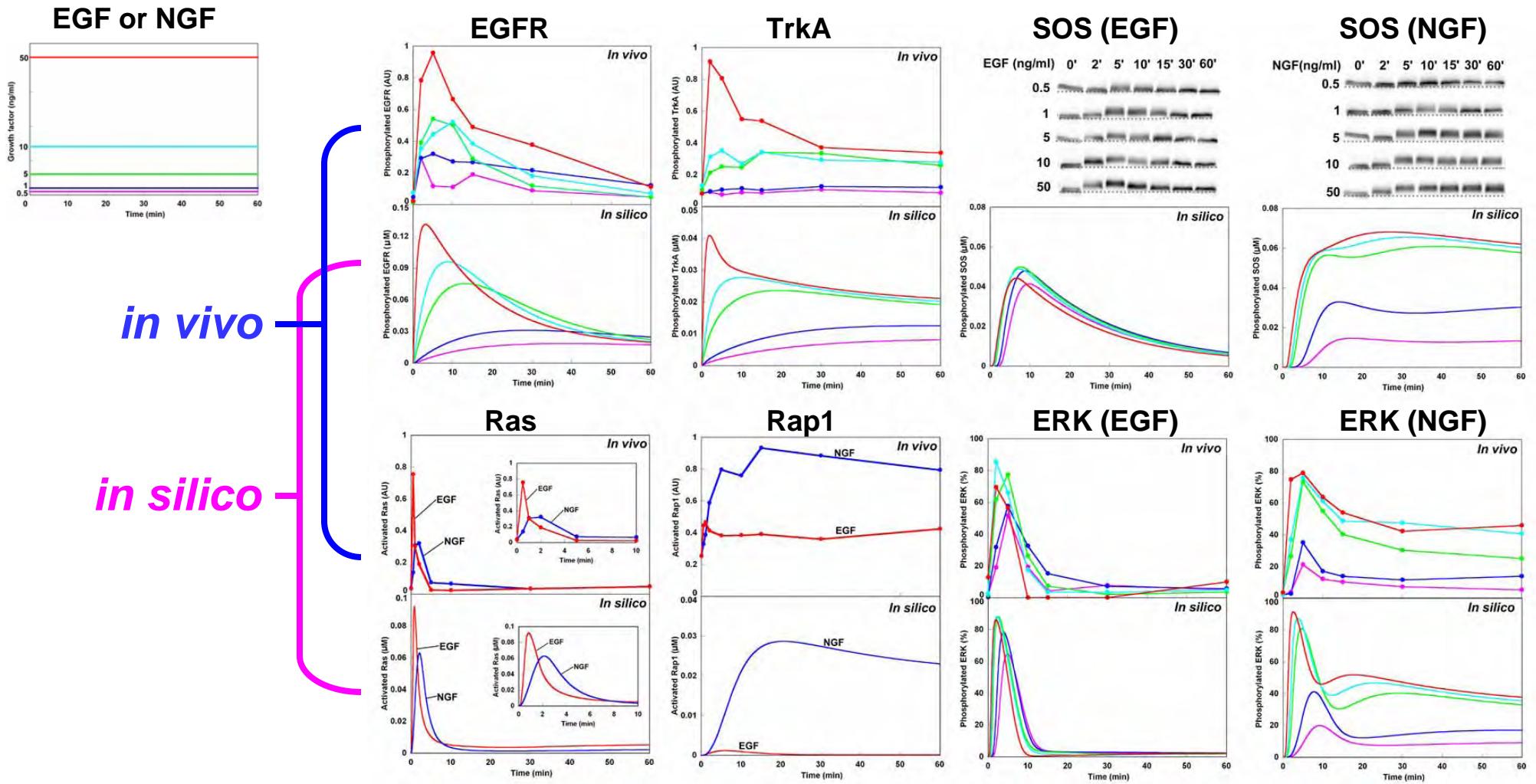


Screenshot of *GENESIS/Kinetikit*



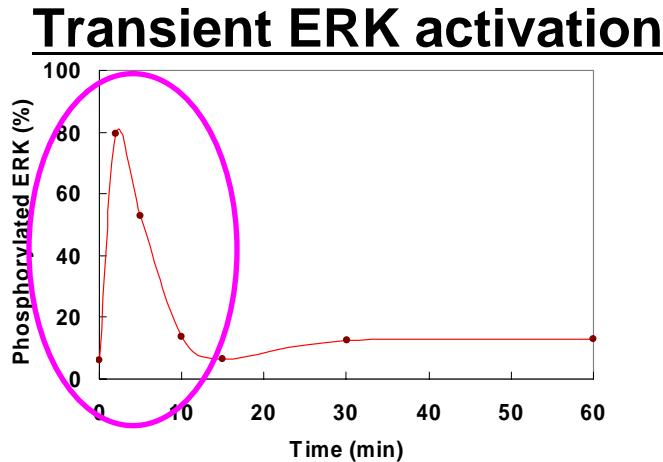
In vivo dynamics were measured.

In vivo and in silico temporal dynamics of ERK signaling networks

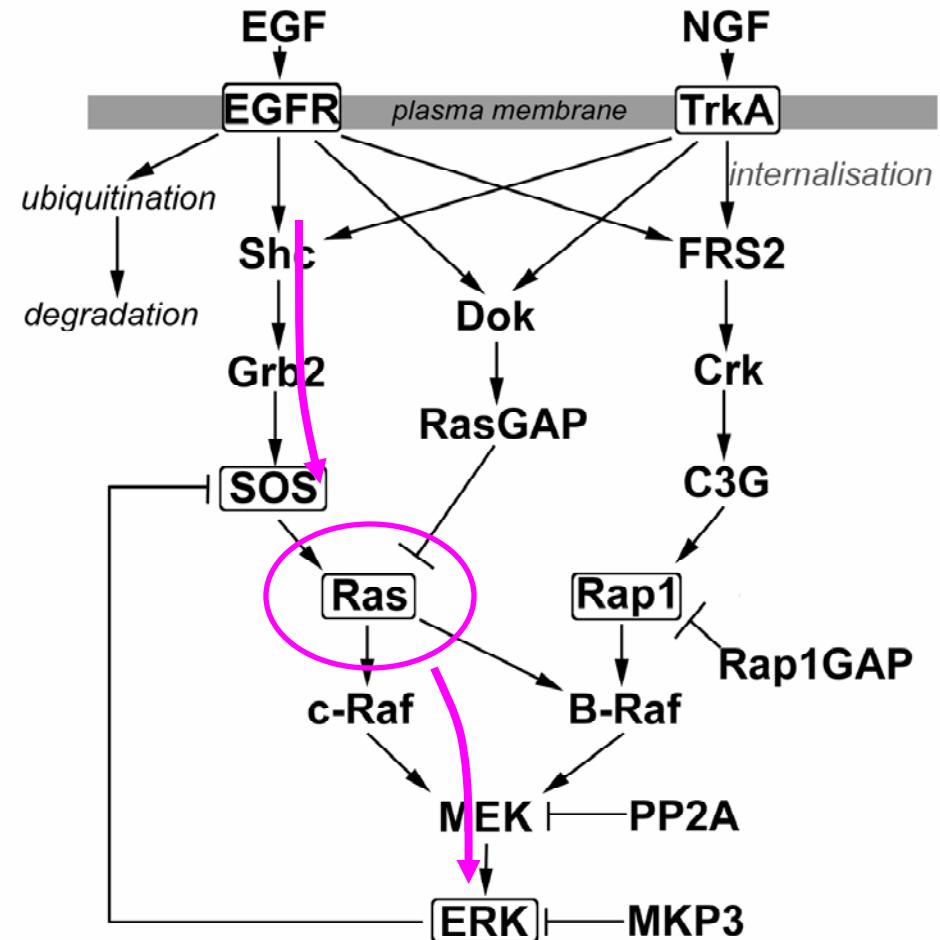
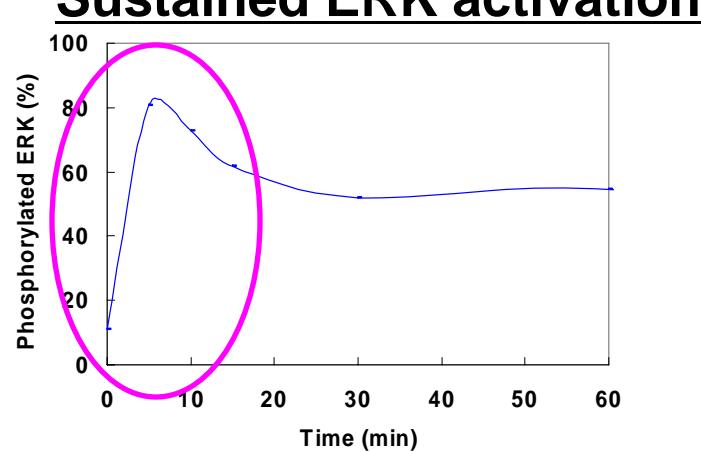


Transient Ras and ERK activation

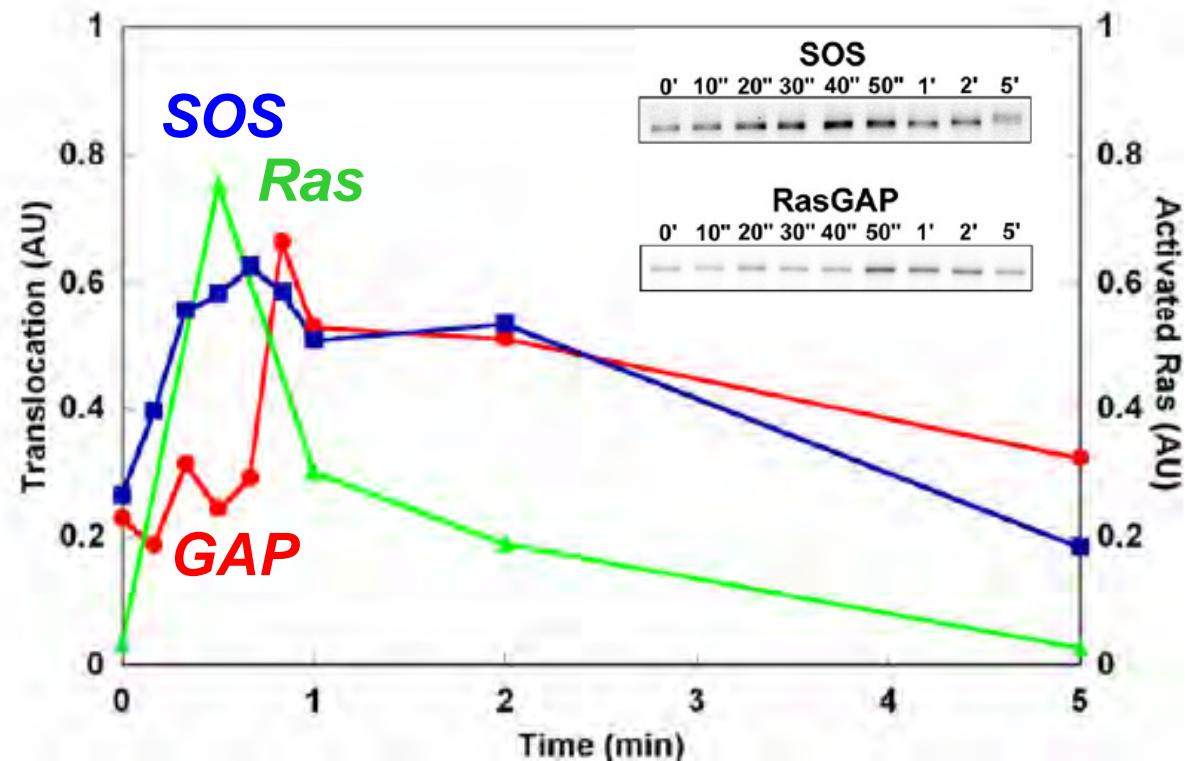
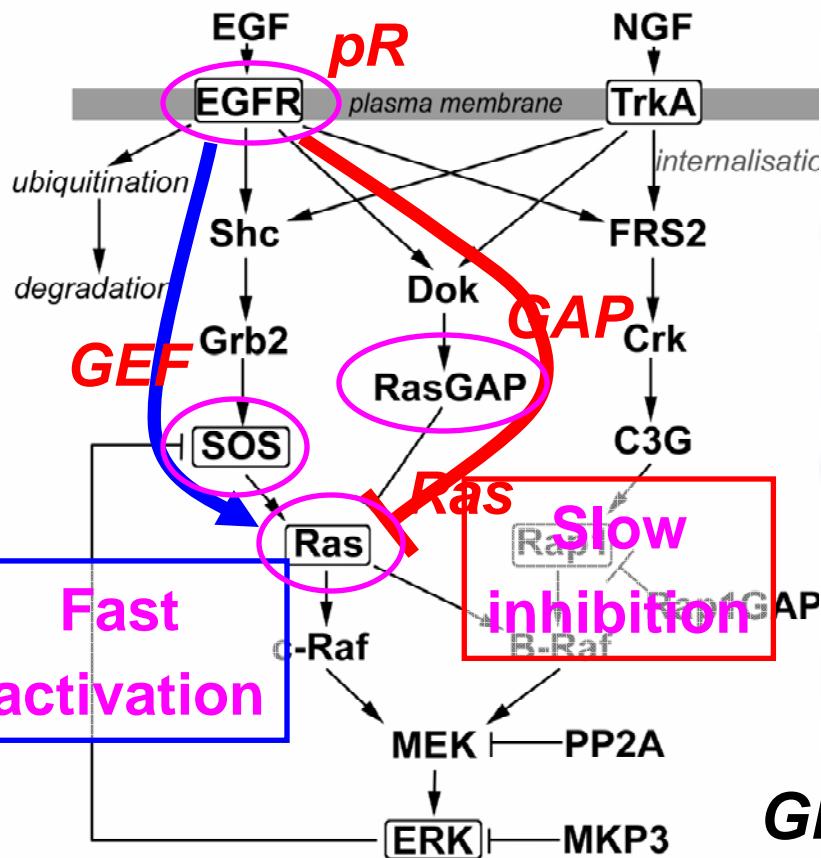
EGF



NGF



Transient Ras activation



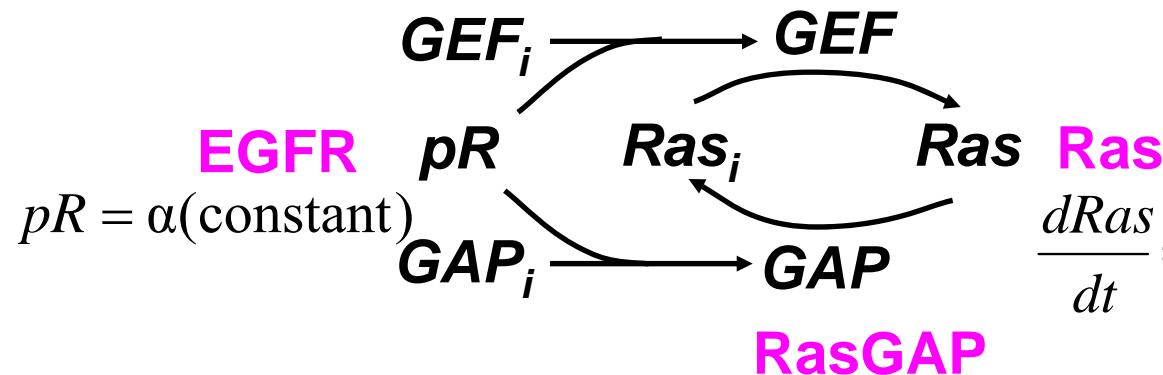
GEF: fast activation GAP: slow inhibition

Transient Ras activation

Simple Model of Ras

$$\frac{dGEF}{dt} = k_2 \{ pR - (1 + pR) GEF \}$$

SOS



$$pR = \alpha(\text{constant})$$

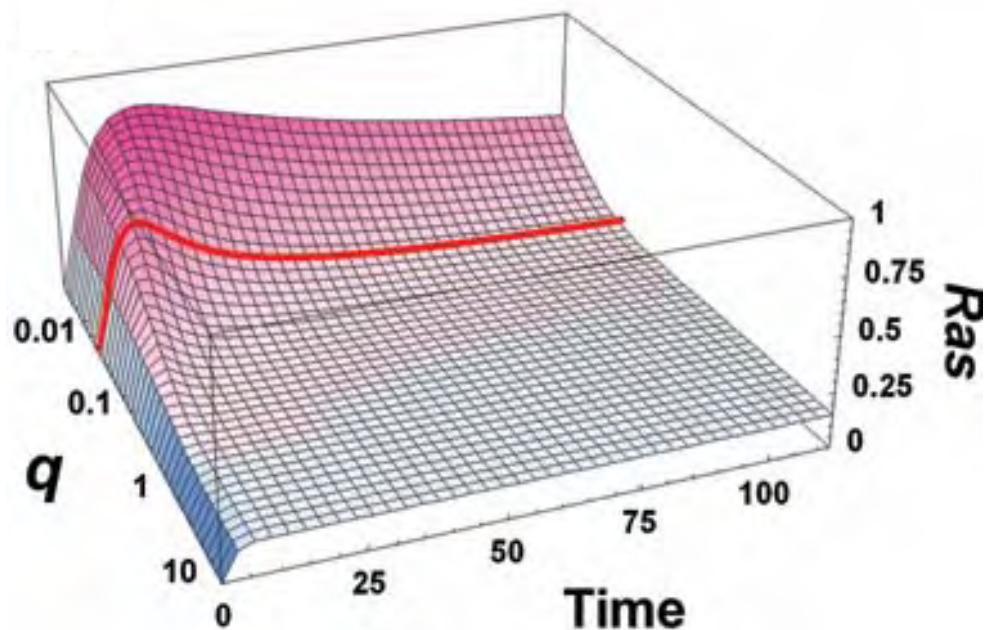
$$\frac{dRas}{dt} = k_6 [\text{GAP}_{\text{total}}] \left\{ \frac{GEF}{K_e} - \left(\frac{GEF}{K_e} + \text{GAP} \right) Ras \right\}$$

$$\frac{dGAP}{dt} = k_4 \{ p \cdot pR - (1 + p \cdot pR) GAP \}$$

The relative time constant of GAP to GEF $1/q = k_4/k_2$

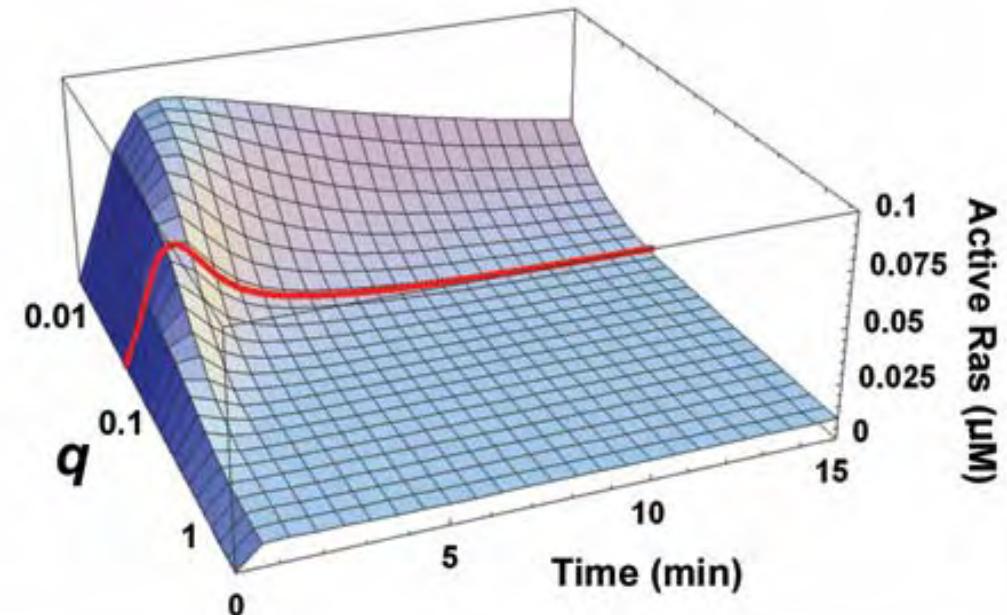
$q < 1$, **GEF is faster**; $q > 1$, **GAP is faster**

Simple Model of Ras



Simple Ras model

- $q < 1$: GEF is faster
Transient Ras activation ○
- $q > 1$: GAP is faster
Transient Ras activation ×



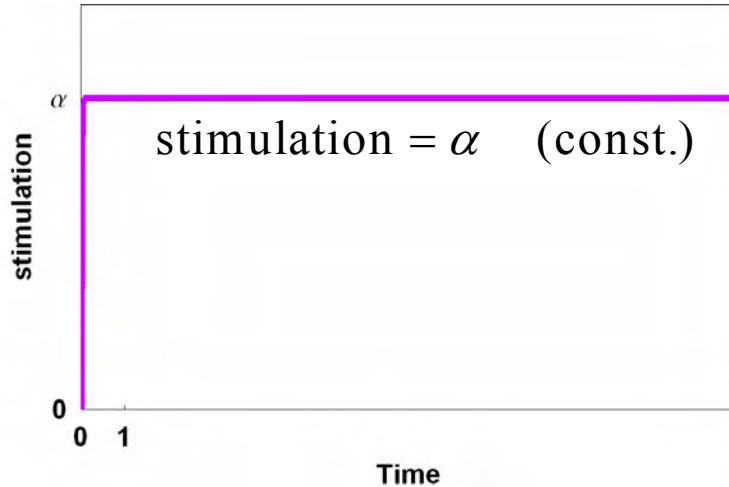
***In silico* model**

- $q < 1$: GEF is faster
Transient Ras activation ○
- $q > 1$: GAP is faster
Transient Ras activation ×

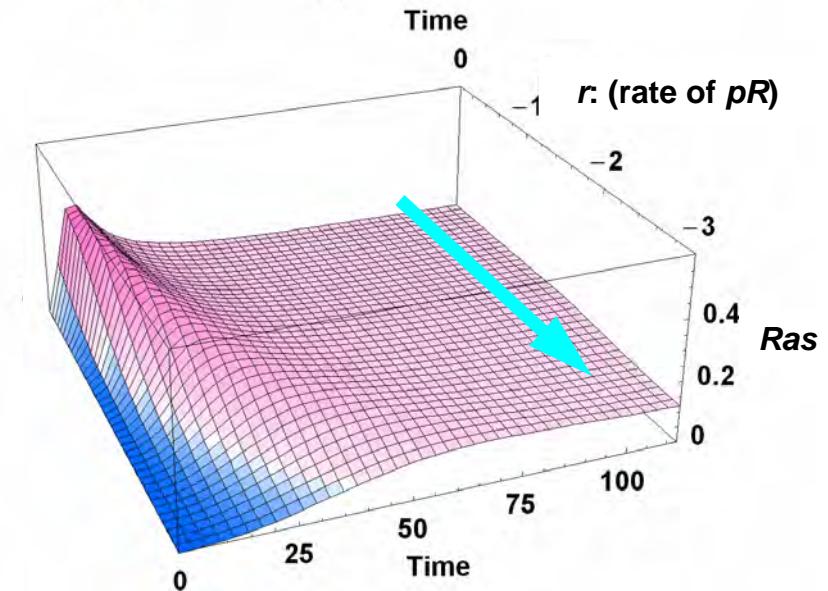
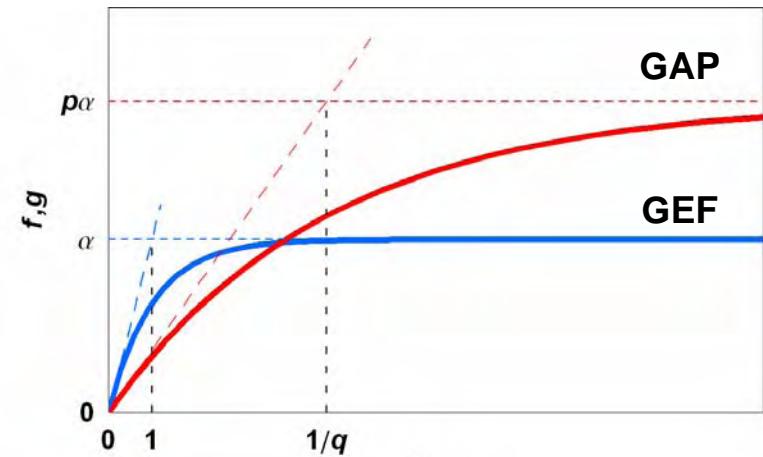
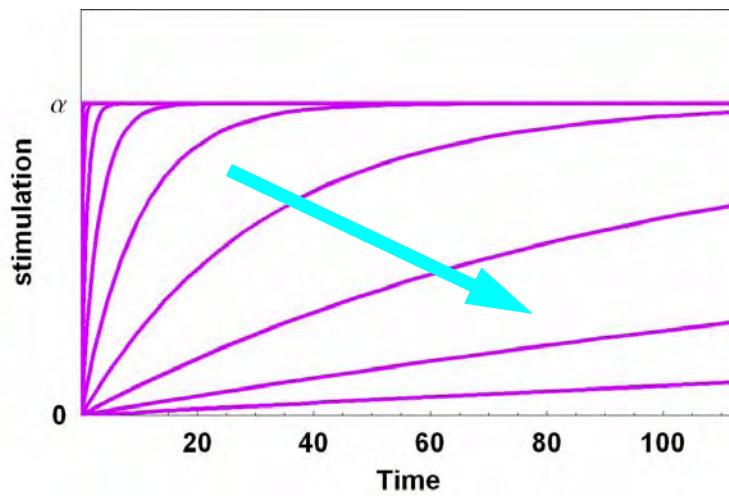
Ramp stimulation

- How to change the relative time constant, q , in vivo-

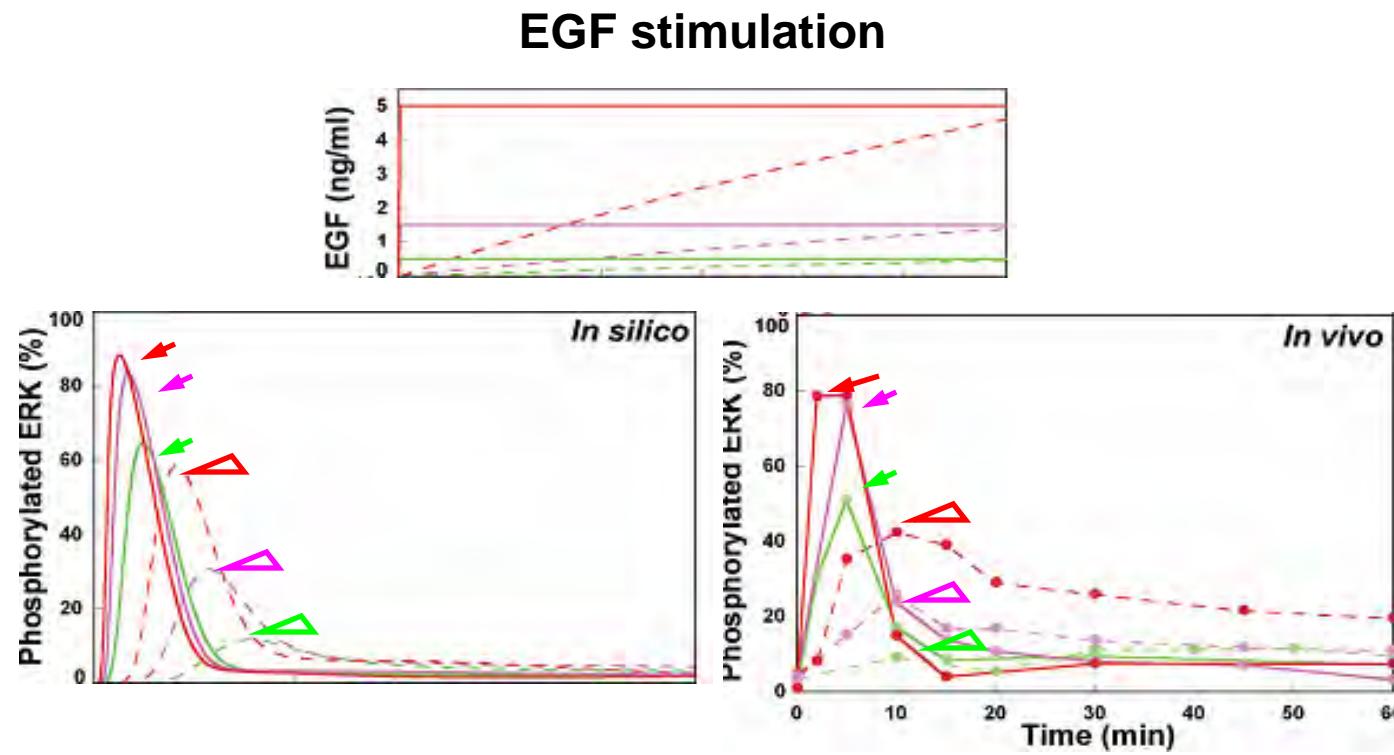
Step



Ramp

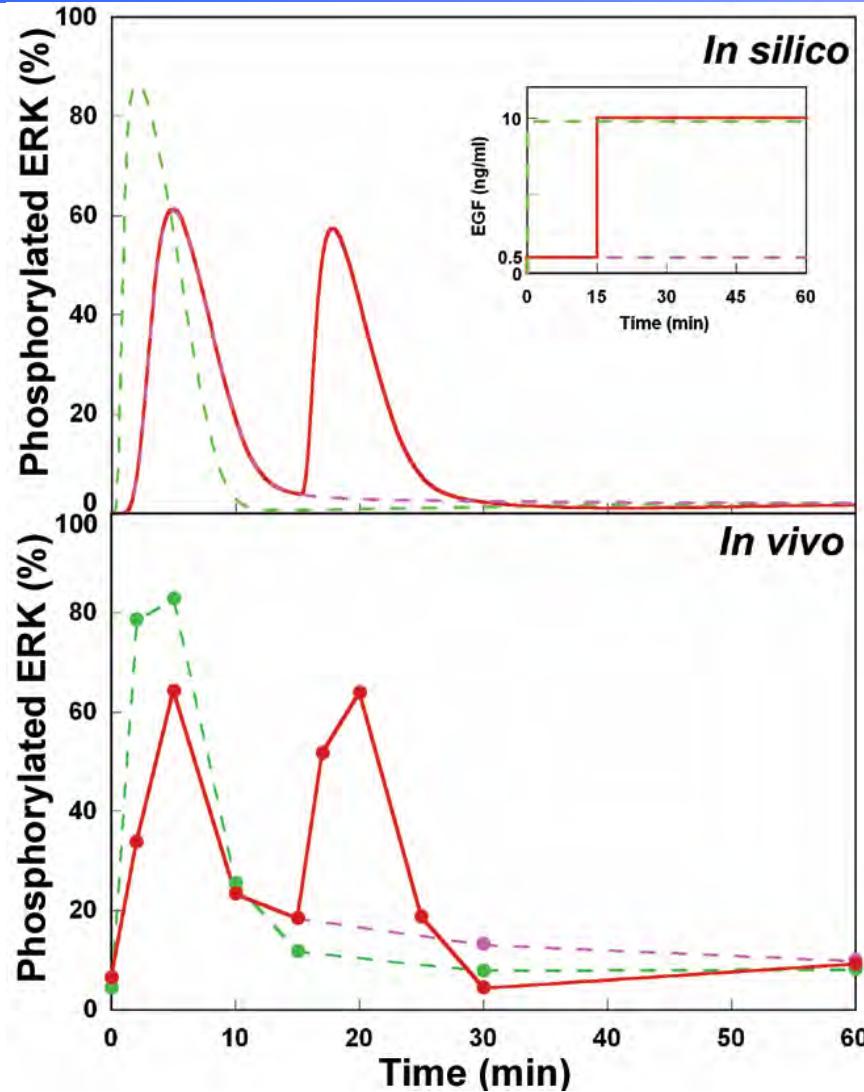


ERK dynamics respond to ramp stimuli



Ras system specifically captures temporal rate of EGF.

*Stepwise increase of EGF *in vivo* and *in silico**



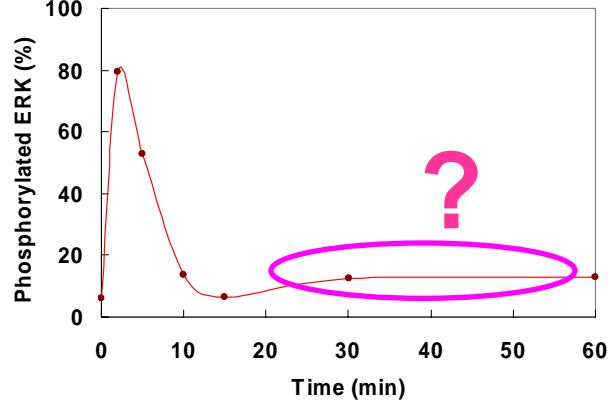
Rapid temporal rate
Difference in concentration

Threshold or absolute concentration

Dynamics of ERK networks

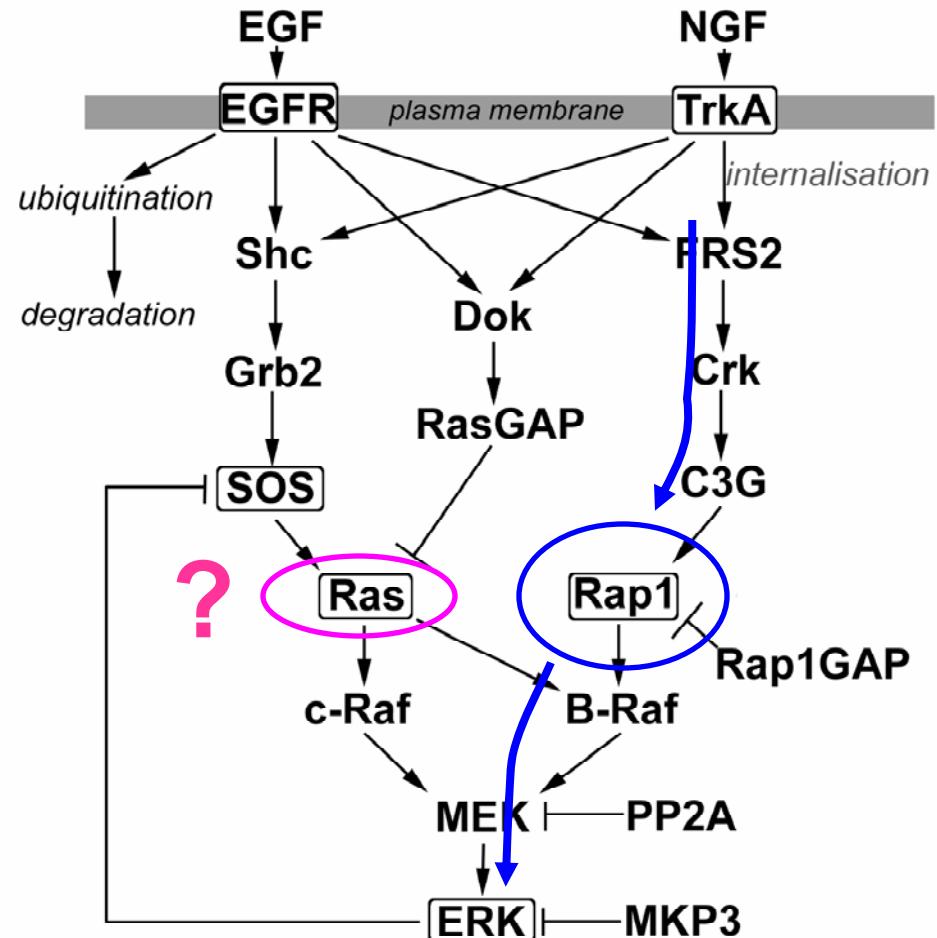
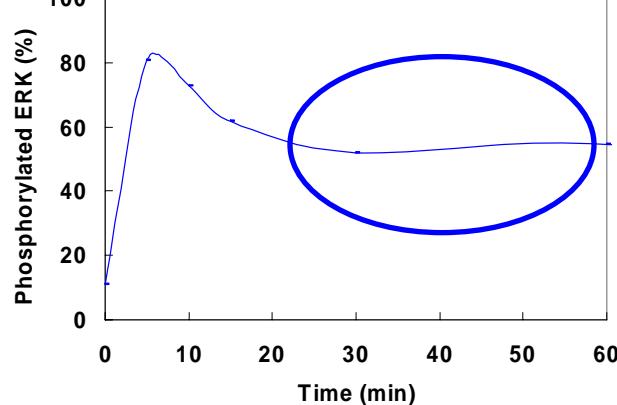
EGF

Transient ERK activation

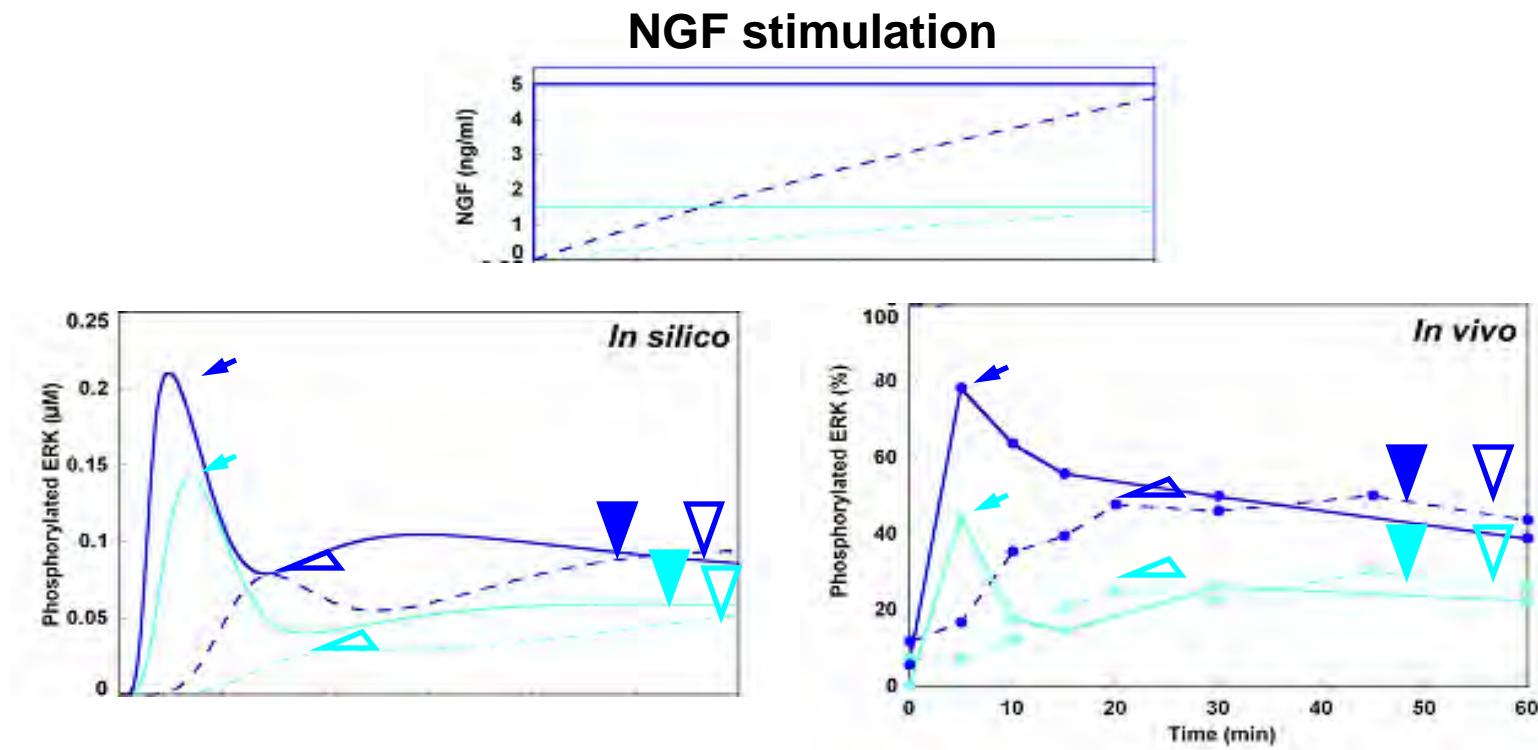


NGF

Sustained ERK activation

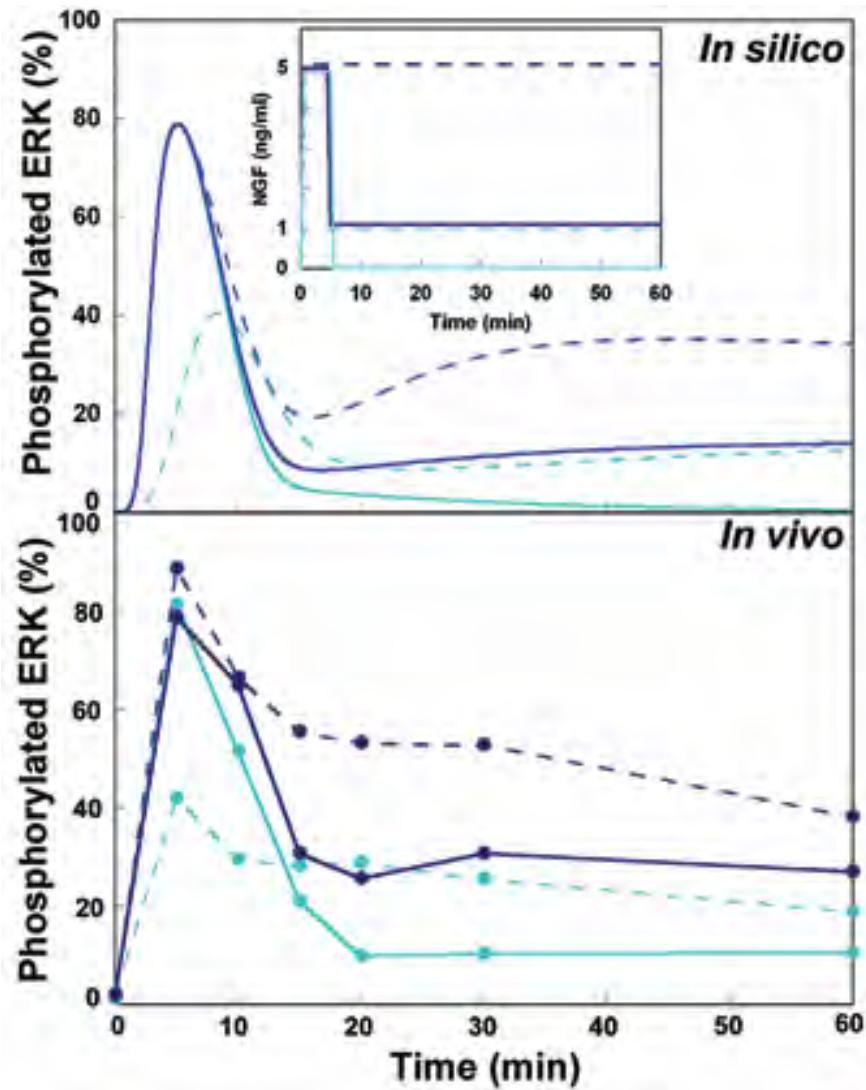


ERK dynamics respond to ramp stimuli



Sustained ERK activation → final concentration of NGF

*Stepwise decrease of NGF *in vivo* and *in silico**



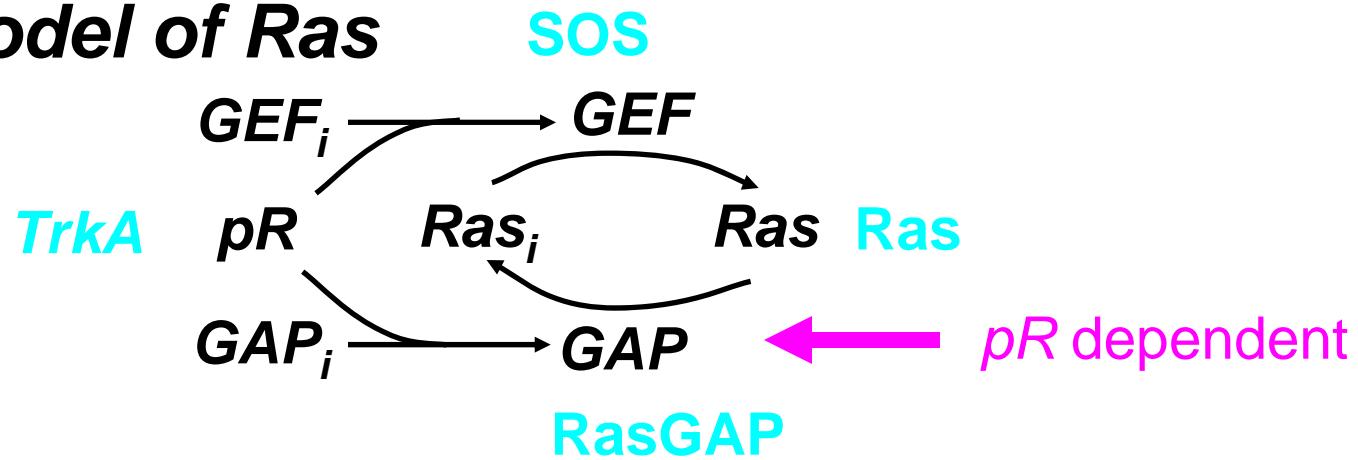
Final concentration

~~Initial concentration~~

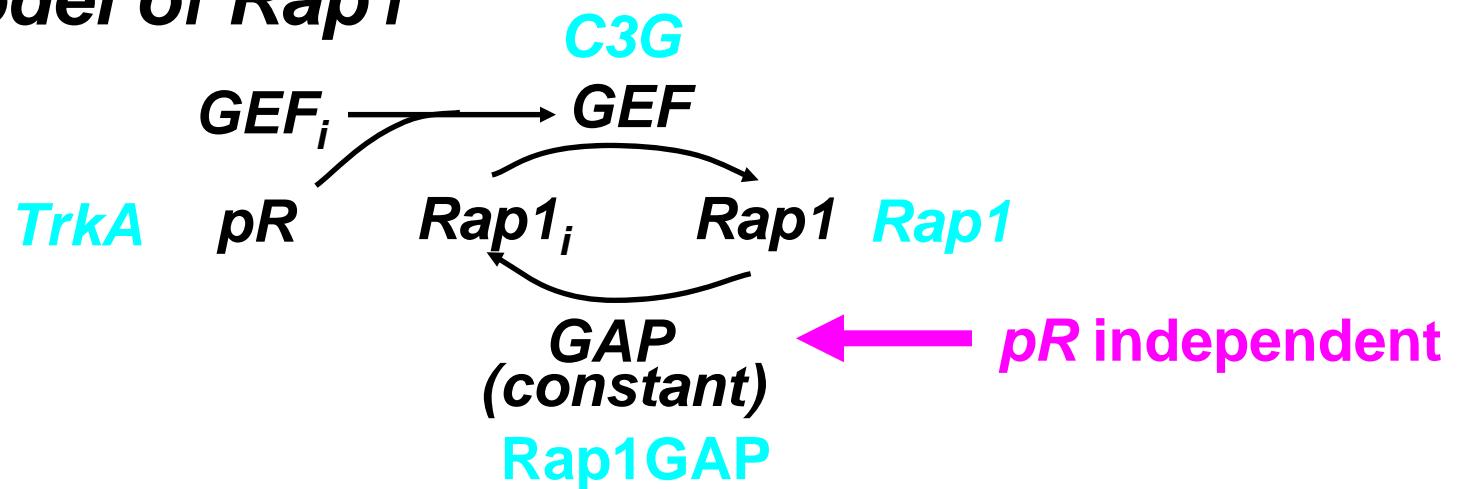
~~Temporal rate~~

Simple Model of Rap1 and Ras

Simple Model of Ras



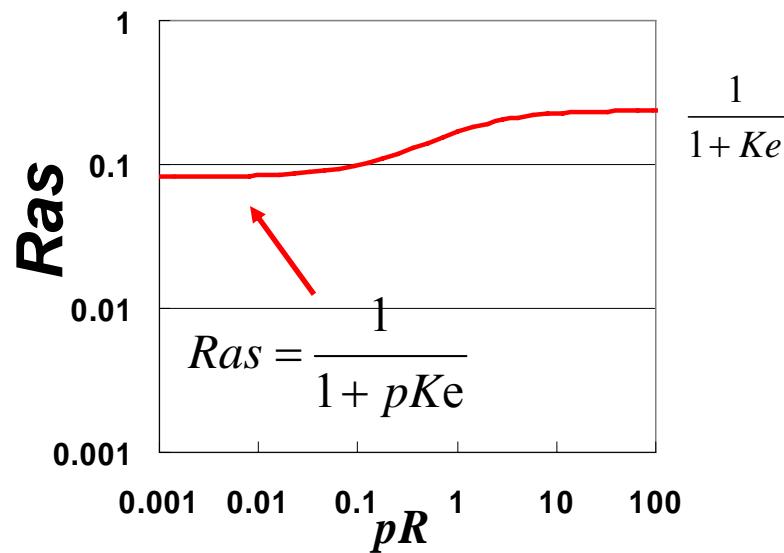
Simple Model of Rap1



Ras and Rap1 at steady state

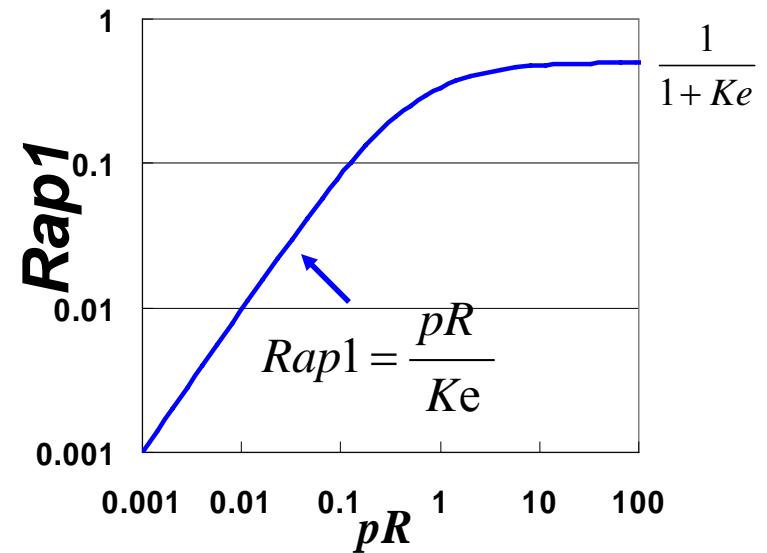
Ras

$$Ras = \frac{1}{1 + pKe \frac{1 + pR}{1 + p \cdot pR}}$$

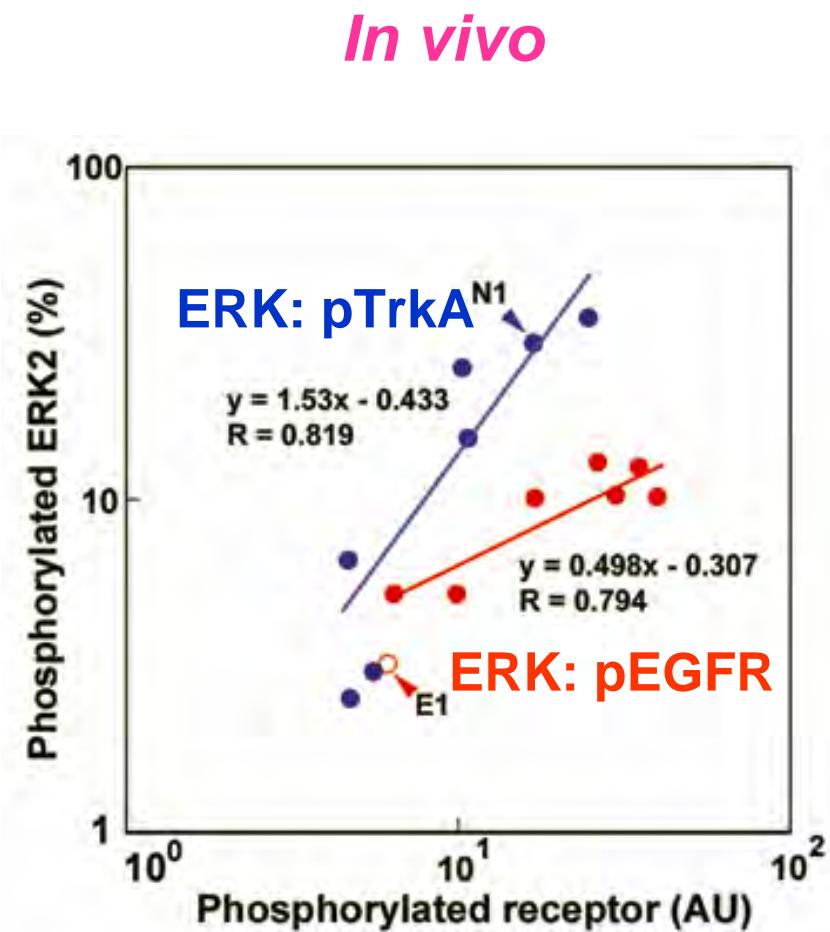
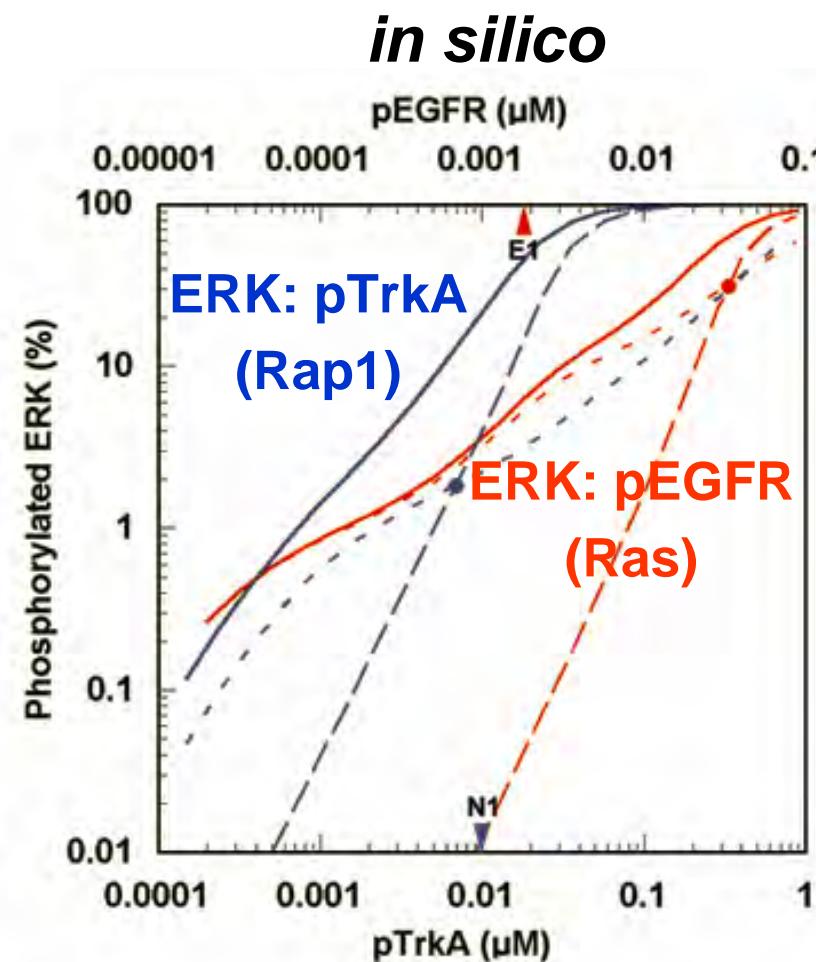


Rap1

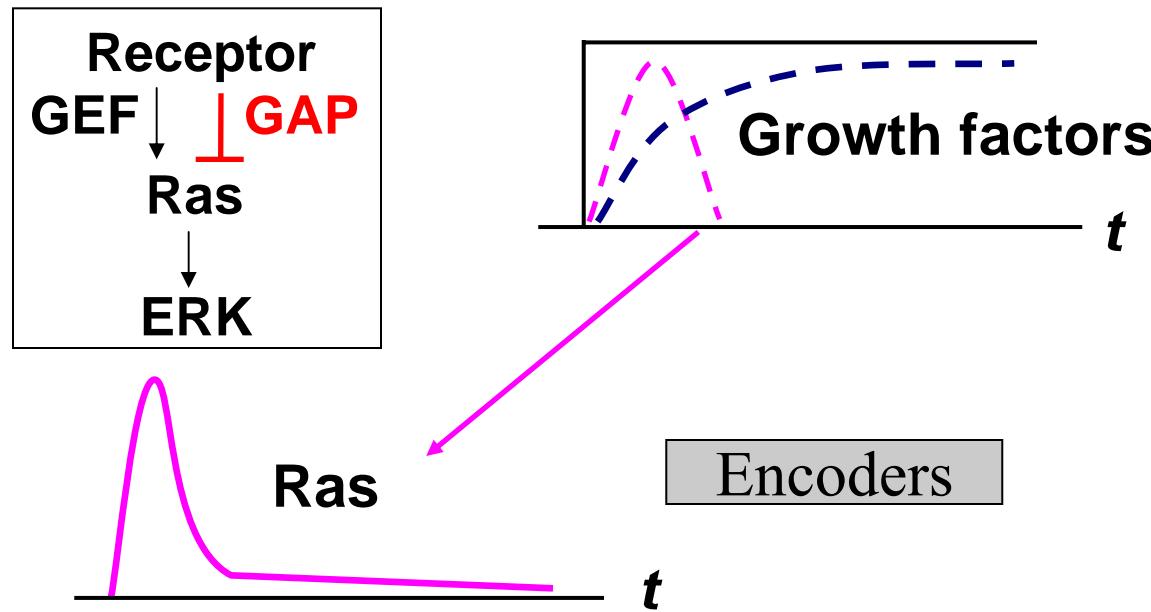
$$Rap1 = \frac{pR}{(1 + Ke)pR + Ke}$$



Sustained ERK activation against EGFR or TrkA in silico and in vivo

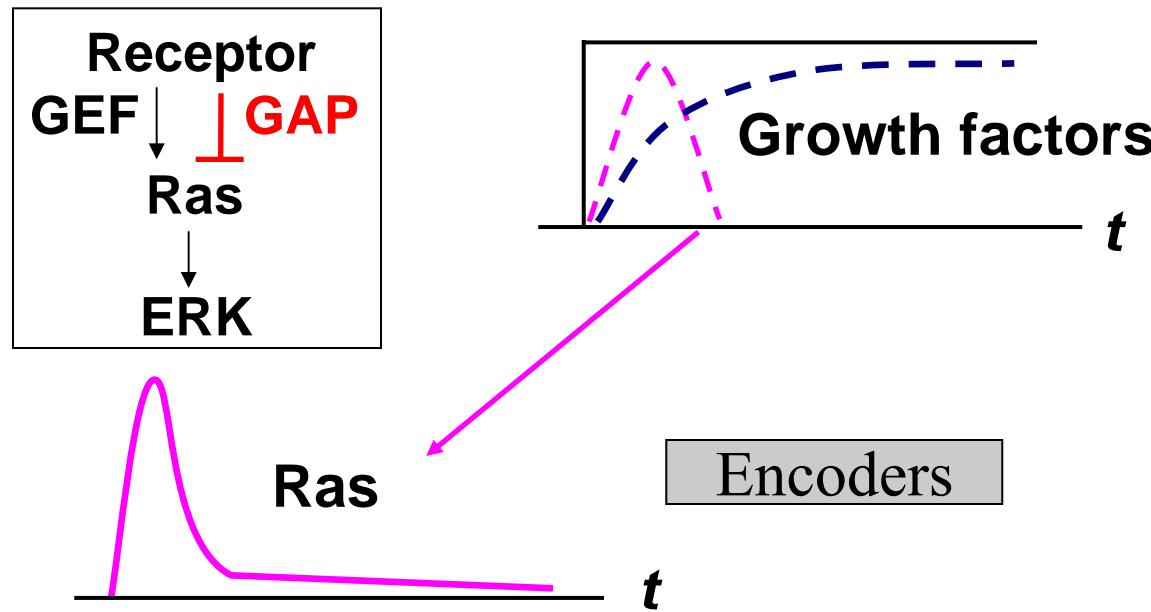


Distinct features of the Ras and Rap1 systems



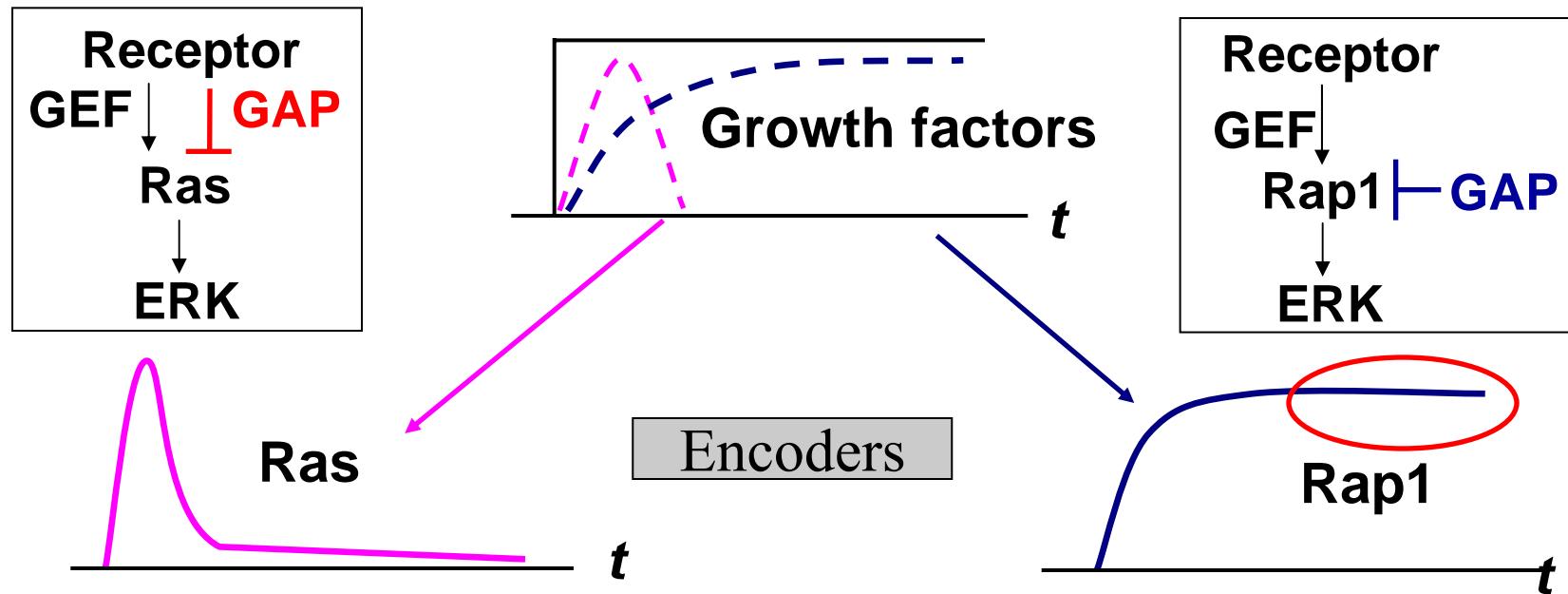
Sasagawa, S. et al, *Nat. Cell Biol.* 2005, 7 (4), 365-373

Distinct features of the Ras and Rap1 systems



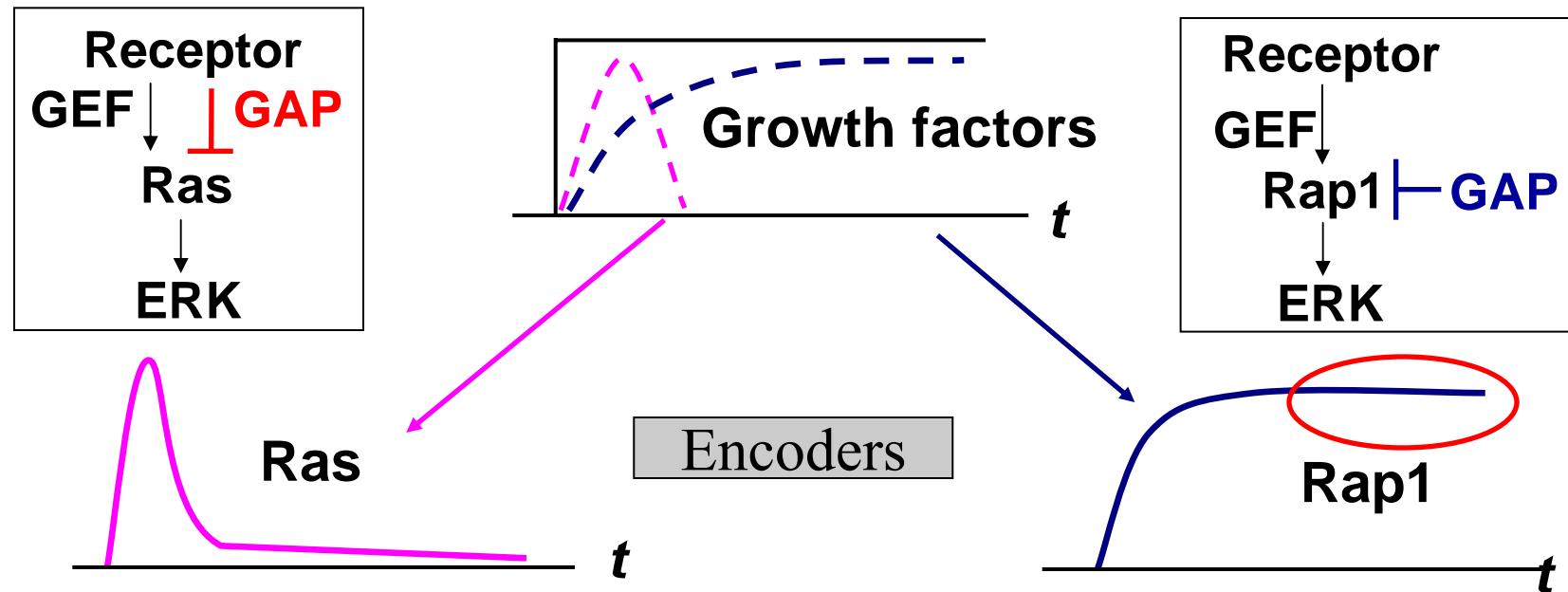
1. **Transient peak: Rapid increase of GF
Rapid temporal patterns**

Distinct features of the Ras and Rap1 systems



1. Transient peak: Rapid increase of GF
Rapid temporal patterns
2. Sustained activation
Independent from GF

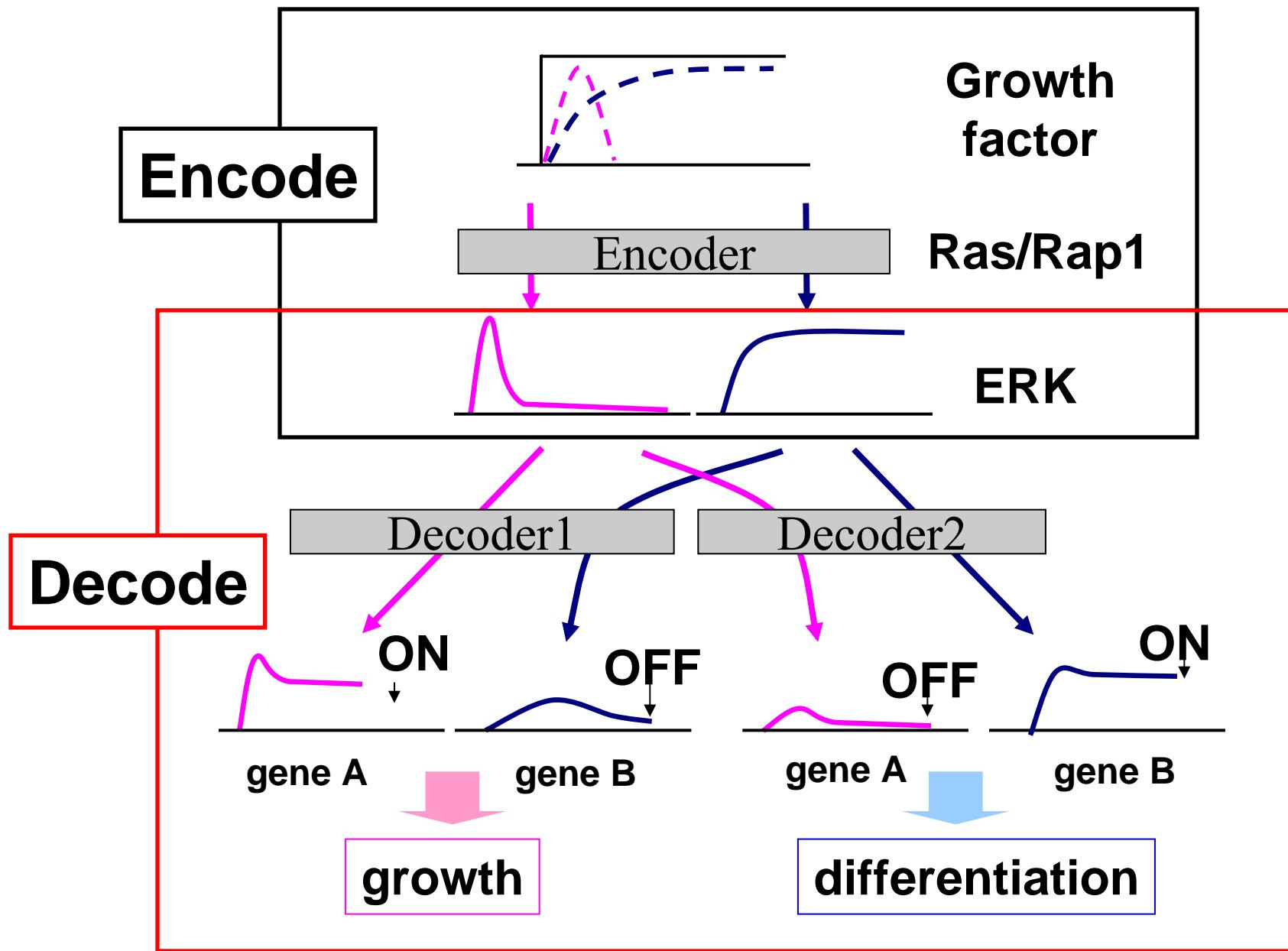
Distinct features of the Ras and Rap1 systems



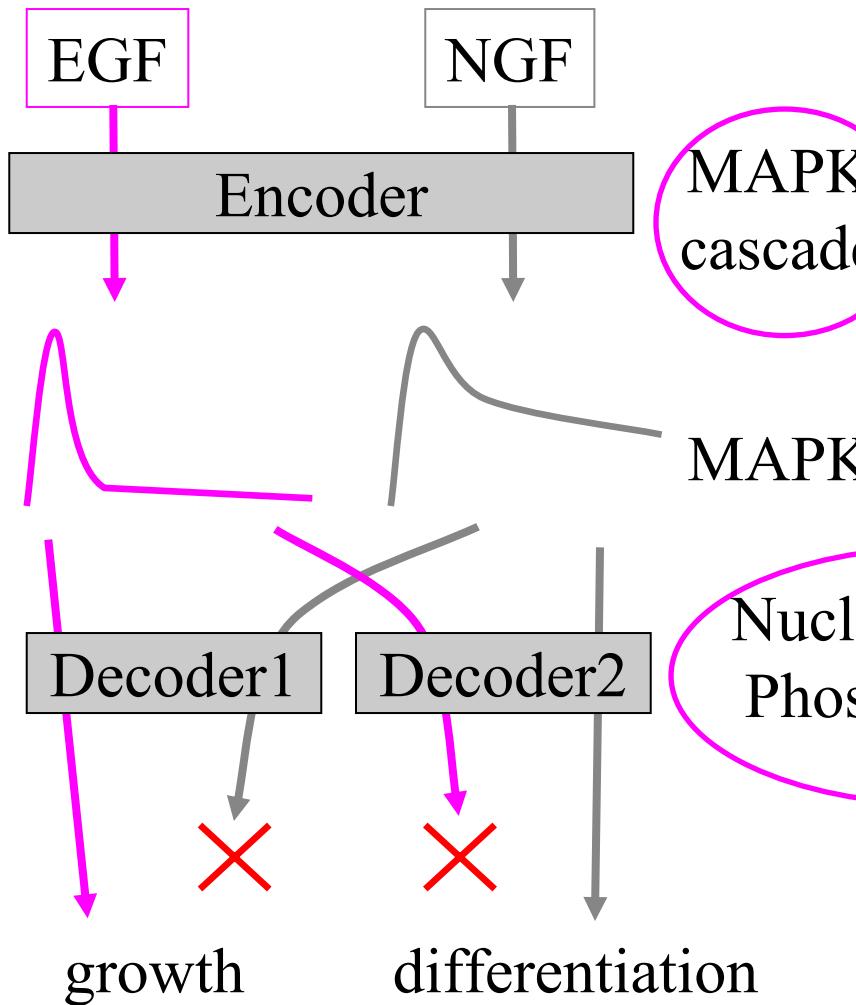
1. Transient peak: Rapid increase of GF
Rapid temporal patterns
2. Sustained activation
Independent from GF

1. **Sustained activation**
Final amplitude of GF
Slow temporal patterns

Temporal coding of ERK signaling networks



Decoding of ERK signaling network



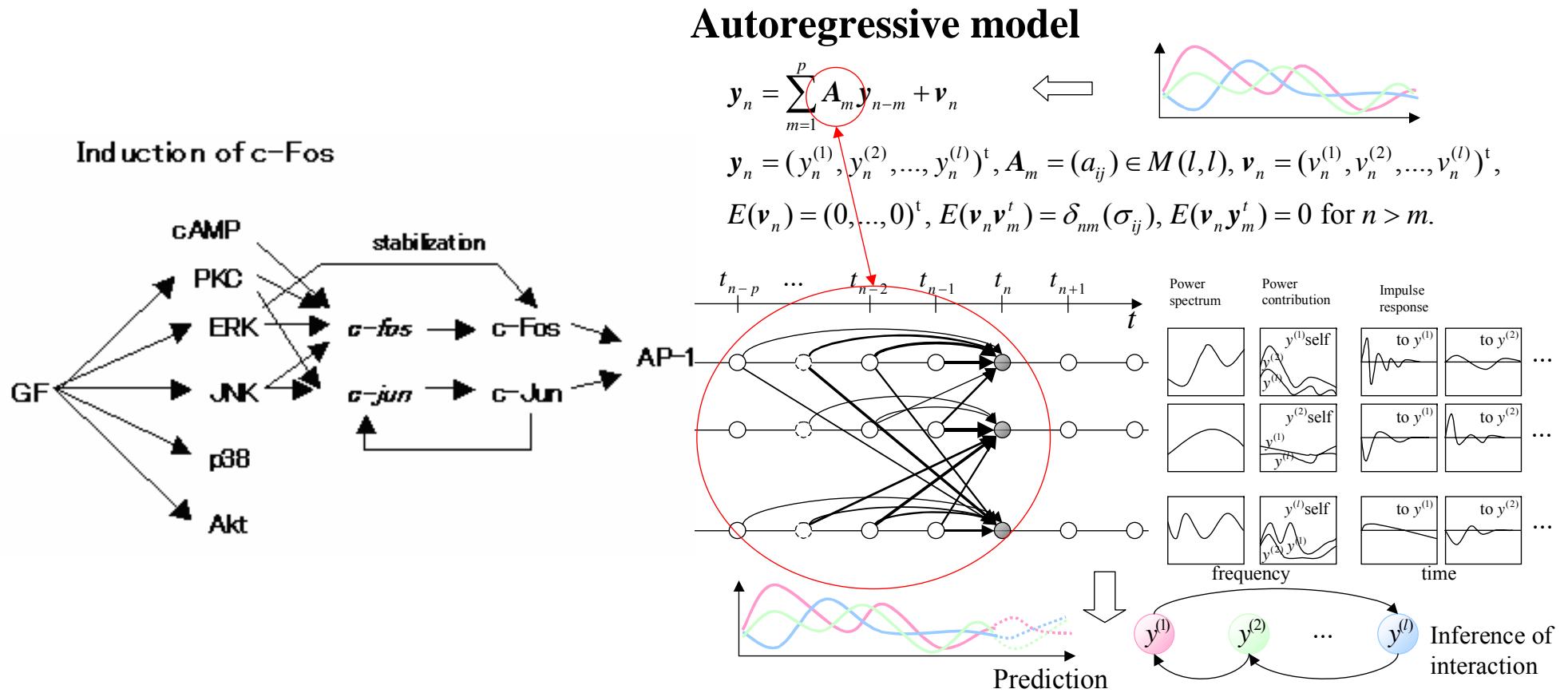
Well-defined network
⇒ Differential equation

Distinct temporal patterns
of ERK should be
differently decoded by
downstream gene
expression

Network is unknown,
but they are related!
⇒ Statistical model

Statistical model of downstream of ERK

Temporal patterns tell the interactions of molecules



Temporal patterns requires high throughput measurements

Minimal requirement of time points for AR model

$$\begin{array}{c} \boxed{0\text{min} \sim 120\text{min}} \\ \times \\ \boxed{4 \text{ Signaling molecules}} \\ \times \\ \boxed{\text{GF dose } \times 3} \\ \times \\ \boxed{n=3} \end{array}$$

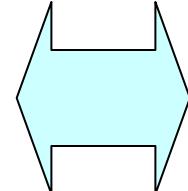
= 1116 points !

Automation by Robots + multiple immunostaining
= 96well X 6 plates

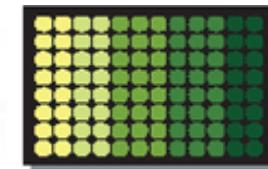
Automatic incubator



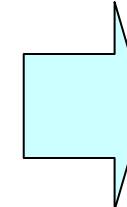
Cell culture
Stimulation
immunostaining



BiomekNX



HTP analysis



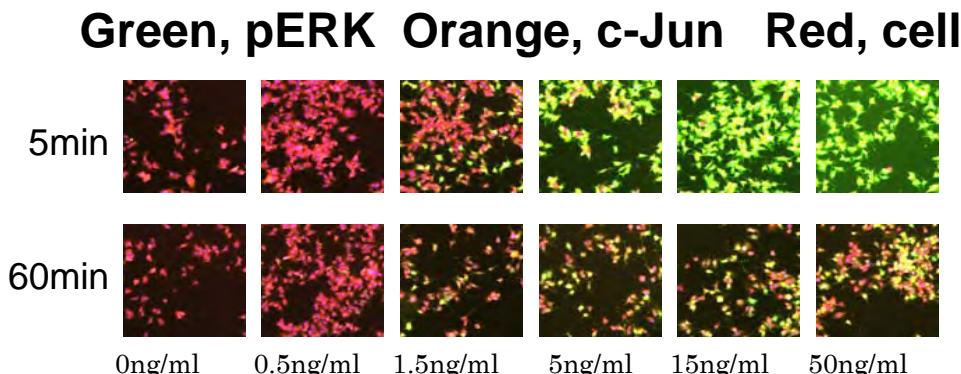
cellWoRx



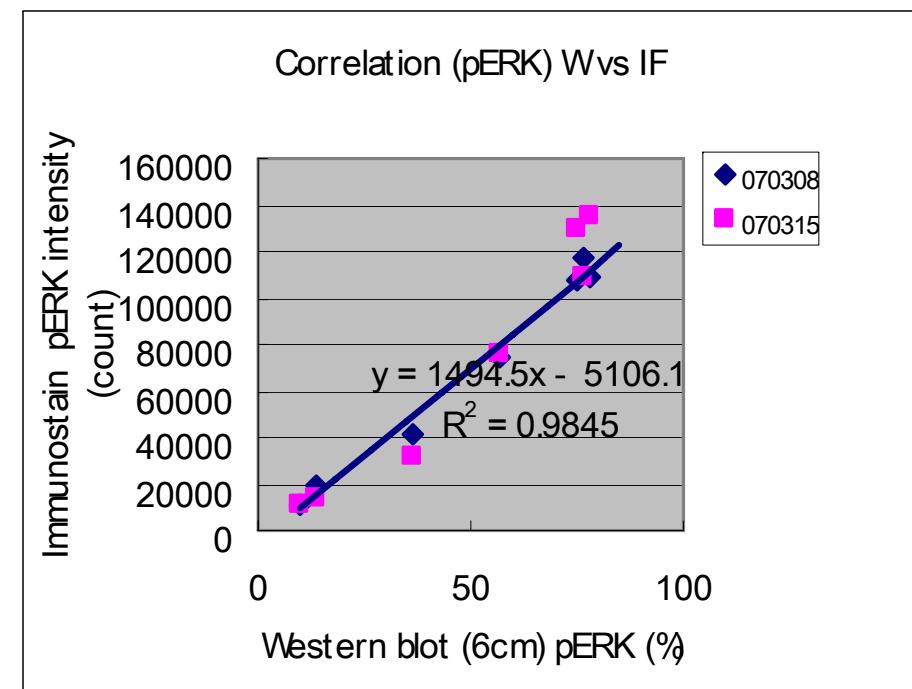
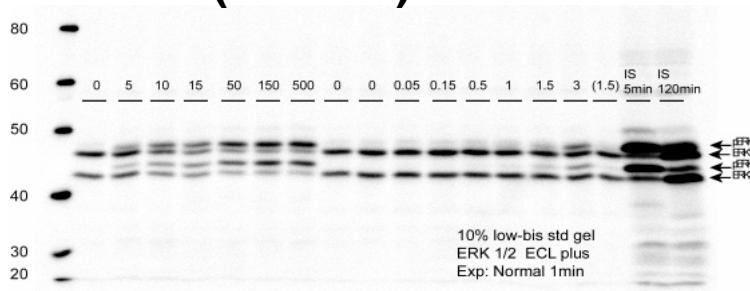
Quantitative measurement of pERK by immunostaining

NGF-induced ERK phosphorylation

Immunostaining (Automatic)



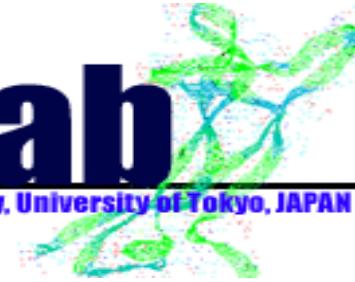
Western blot (manual)



High correlation between WB and IS
→ Quantitative measurement

Kuroda Lab

Undergraduate Program for Bioinformatics and Systems Biology, Graduate School of Information Science and Technology, University of Tokyo, JAPAN



www.kurodalab.org

Hiyoriuki Kubota (Biology)

Yu-ichi Ozaki (Math)

Hidetoshi Urakubo (Physics)

Shinsuke Uda (Statistics)

Kazuhiro Fujita

Jaehoon Chung

Minoru Honda

Yu Toyoshima

Miharu Sato

Risa Kurabayashi

Yoko Shimao

